Alaska Department of Fish and Game
Division of Wildlife Conservation
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Molecular Genetic Approaches in Wildlife Management

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Research Performance Report
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Federal Aid in Wildlife Restoration
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This is a progress report on continuing research. Information may be refined at a later date.

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PROJECT TITLE: Molecular Genetic Approaches in Wildlife Management

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GRANT AND SEGMENT NR.: W-27-4

PROJECT NR.: 1.54

SEGMENT PERIOD: 1 July 2000-30 June 2001

WORK LOCATION: SOLDOTNA

STATE: Alaska

I. PROGRESS ON PROJECT OBJECTIVES

OBJECTIVE 1: Create and maintain a permanent frozen tissue bank and associated database.

Certain area biologists were contacted and provided supplies for collecting and archiving samples from animals they encounter routinely in their duties. (See Job 1)

OBJECTIVE 2: Determine suites of nuclear and/or mitochondrial markers suitable for analysis at the individual and population levels for selected species.

Tentative arrangements were made to participate in a research visit to a USDA lab to investigate the application of single nucleotide polymorphisms (SNPs) to genetic studies of Alaska wildlife. SNPs are extremely abundant biallelic nuclear markers that can be assessed through colorimetric assays, which increases the speed of data acquisition. No SNP markers have been developed for wildlife studies, but we hope to test markers developed for domestic bovids and caprids. (See Job 2)

OBJECTIVE 3: Document genetic variation within and among populations of Alaskan wildlife for forensic and biological purposes.

Levels of genetic variation of elk on Afognak Island were significantly less than current levels in elk from the Olympic Peninsula, Washington, which served as the source of founding individuals for the Alaskan population. Furthermore, levels of variation in both

populations were less that expected based on data from Canadian elk populations. (See Job 4)

OBJECTIVE 4: Develop both field and laboratory methods appropriate to conduct molecular-based CMR population analyses.

Discussions with colleagues who are experimenting with this technique have led to the decision to abandon fecal analysis, for the moment, and concentrate on hair as the DNA source for surveys. A novel hair-collection device will be tested at the Moose Research Center this year. (See Job 5)

II. SUMMARY OF WORK COMPLETED ON JOBS IDENTIFIED IN ANNUAL PLAN THIS PERIOD

JOB 1: Develop and maintain a frozen tissue collection and characterize genetic variability in populations of Alaska's game species.

Supplies for archiving tissue samples were purchased and sent to those area biologists who have agreed to collect samples opportunistically in the normal course of their duties.

JOB 2: Genetic differentiation of Alaskan caribou herds. (in collaboration with Patrick Valkenburg, ADF&G, Fairbanks)

Results from two years of sampling were generated at a lab at the University of Alberta. Unfortunately, only summary statistics for one year have been transmitted by that lab. We are attempting to retrieve the raw data so that we may begin our own analyses.

A proposal is being prepared to justify a research visit to a USDA lab for assessment and development of SNP markers that would be effective for discrimination among caribou herds and applicable to genetic studies of other cervids.

JOB 3: Moose population genetics.

No progress was made on this job.

JOB 4: Assess inbreeding in elk from Afognak and Raspberry Islands (in collaboration with Larry van Daele, ADF&G, Kodiak)

Elk tissue samples from Afognak Island and the Olympic Peninsula, Washington were sent to a commercial genetics laboratory (Wildlife Genetics International, Edmonton, Alberta) for determination of genotypes at microsatellite loci. That lab has developed a suite of 16 microsatellite markers for use in pedigree analysis in farmed elk. I sought to add those markers to our analysis of founder effect in Afognak elk because the some of the 10 loci I analyzed previously did not amplify well enough to include in the analysis. Therefore, fewer loci were used in the analysis than I had planned, which reduced the statistical power for testing the hypothesis.

A minimum of 11 loci were scored in all samples, and at least 15 loci were scored successfully for 51of 56 elk tissue samples. All loci were polymorphic, with numbers of

alleles per locus ranging from 2 to 6. Mean number of alleles per locus was 4.0 for all samples combined, 3.75 for Olympic Peninsula samples, and 3.0 for Alaska samples. The number of loci exhibiting private alleles (alleles shared with no other population) were 2 for Alaska and 11 for Olympic Peninsula. No loci deviated significantly from Hardy-Weinberg equilibrium in either population, but each population exhibited some degree of gametic phase disequilibrium. Pairs of loci in disequilibrium were not consistent between populations, which suggests that the disequilibrium is caused by demographic processes rather than linkage. An exact test of population differentiation revealed significant ($P < 0.05$) genic differentiation between the two populations at 10 of 16 loci (no correction for multiple comparisons) and highly significant ($P < 0.00001$) differentiation across all loci. I conclude that the Afognak population of elk suffered a founder effect as a result of a low number of animals included in the transplant.

Interestingly, both populations showed less allelic diversity than generally observed in elk populations in Canada (D. Paetkau, pers. comm.). That observation may be indicative of a founder effect or historic bottleneck in the Olympic Peninsula population, which has been amplified through the transplant to Alaska. This serial reduction of genetic diversity can result in populations that are unable to adapt to changing environmental conditions, and illustrates a potential hazard involved in transplants. Assessing the genetic diversity of candidate source populations can ensure that appropriate levels of genetic diversity are maintained in transplanted populations.

JOB 5: Molecular-based CMR Technique Development

I consulted with biologists attempting to use this technique in other areas and with other species, hoping to incorporate their experiences into my research. They generally stated that extraction and amplification of DNA from fecal matter is problematic. Although some successes have been reported in the literature, this technique is viewed with suspicion. The use of hair as the DNA source, however, seems to provide much higher rates of success. The primary concern with that technique involves random sampling of hairs from the population, and preventing contamination of samples due to sampling of multiple individuals. One design that is being used on bears in British Columbia (G. Mowat, pers. comm.) seems to show promise for moose. The sampling apparatus is a piece of barbed wire strung across a trail at chest height. One end of the wire is attached to an elastic strap and the other is attached to monofilament line of appropriate strength. As the animal encounters the wire on the trail, the barbs remove and retain some of the hair. The strength of the monofilament is selected so that it breaks as the animal attempts to move forward past the obstruction, and the elastic strap pulls the wire out of the path so it has little chance of sampling future animals. I intend to test such a device at the Moose Research Center during the next reporting period.

JOB 6: Prepare annual and final reports.

III. ADDITIONAL FEDERAL AID-FUNDED WORK NOT DESCRIBED ABOVE THAT WAS ACCOMPLISHED ON THIS PROJECT DURING THIS SEGMENT PERIOD

Two manuscripts were prepared from data collected on a previous project dealing with 1) mitochondrial genetic diversity and historic demographics of moose worldwide and the

implications of those data on diversity of present-day populations; and 2) regional differences in diversity of North American moose populations and the implications for relationships among those populations and suitability of current taxonomic designations.

IV. FEDERAL AID TOTAL PROJECT COSTS FOR THIS SEGMENT PERIOD

$ _54,300

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